KDR-1

Kylie Rika

From: Kylie Rika
Sent: Friday, 9 February 2018 9:27 AM
To: Justin Howes
Subject: FW: Auto-microcons

Hi Justin

This is a concern.

I guess it's one thing for the QPS to understand this risk (if they do) but it's not full testing/disclosure for the case from our lab.

Perhaps the process needs to be re-assessed?

thanks

Kylie Rika Dip Mgt BSc PGrad Dip (Forensic)
Senior Reporting Scientist – Forensic Reporting and Intelligence Team

Forensic DNA Analysis | Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

[redacted]

From: Emma Caunt
Sent: Thursday, 8 February 2018 4:56 PM
To: Kylie Rika
Subject: RE: Auto-microcons

Hi Kylie

I understand from a conversation with Justin that the DNA Insuff process will continue as per the no DNA detected process so samples won't be assessed taking into account the circumstances of the case. I just want to pass on one example.

Rape case
Nothing on the SAIK
Underpants – EFRAC had auto microcon and gave 2 pers mixture of complainant and defendant
Only other sample in the case was defendant on a shoe found in a park
In this case the auto-microcon gave the only evidence to substantiate the claims of the complainant

[redacted]

Thanks

Emma

From: Emma Caunt
Sent: Thursday, 8 February 2018 9:37 AM
To: Justin Howes
Cc: Kylie Rika
Subject: RE: Auto-microcons

Hi Justin

I've been thinking about this a bit more. I want to say from the outset that I am not necessarily opposed to stopping the auto-microcon process, but I do think that there is a risk that we are able to manage.

I am assuming that the 'DNA insuff for processing' line will be added automatically and that it will be added to a list for validation. My question is, how will the validation process be managed?

My personal opinion is that the line should not be validated until the whole case has been assessed to see if processing of this sample would be of benefit, particularly as the quant value reaches the upper range. Obviously at the statement stage, the reporter can assess these samples, but the gap will be if no statement is requested. Since we case manage on a sample by sample basis the 'DNA insuff' results won't be monitored during the normal case management process.

Thanks

Emma

From: Justin Howes
Sent: Wednesday, 7 February 2018 4:14 PM
To: Emma Caunt
Cc: Kylie Rika
Subject: RE: Auto-microcons

Hi, yes I will be changing the expanded comment as I know it is not exactly what we mean. The wording will be similar to the statement wording and making it clear that requests can be actioned.

QPS will have their processes expanded to enable this as well as including how to request further work. The expanded comment change will be added to the current SOP as a comment.

JAH

Justin Howes
Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**

[redacted]

From: Emma Caunt
Sent: Wednesday, 7 February 2018 4:07 PM
To: Justin Howes
Cc: Kylie Rika
Subject: RE: Auto-microcons

Hi Justin

I've had a look at the reports for this and, NCIDD aside, it shows that 10% of samples that went through the auto-microcon gave interpretable results.

The expanded comment for the 'DNA Insufficient for further processing' line states the following:

> This item/sample was submitted for DNA analysis; however the amount of DNA detected at the quantitation stage indicated the sample was insufficient for further processing (due to the limitations of current analytical and interpretational techniques). No further processing was conducted on this item. Please contact Forensic DNA Analysis if further information is required.

This indicates to scientific staff that there is nothing further that can be done with this sample, which is not the case for 10% of samples. It also does not give them the option to request for this sample to be processed further. Can I request that we update the expanded comment to be clear that there may be a chance of getting a usable profile and that they have the option of requesting this? We should probably bring this expanded comment in line with your suggested statement wording as they say different things.

Thanks

Emma

From: Justin Howes
Sent: Wednesday, 7 February 2018 3:18 PM
To: Adrian Pippia; Alicia Quartermain; Allison Lloyd; Amanda Reeves; Angela Adamson; Angelina Keller; Anne Finch; Cassandra James; Claire Gallagher; Deborah Nicoletti; Emma Caunt; Hannah Pattison; Helen Williams; Ingrid Moeller; Jacqui Wilson; Josie Entwistle; Justin Howes; Kylie Rika; Lisa Benstead; Matthew Hunt; Penelope Taylor; Rhys Parry; Sharon Johnstone; Susan Brady; Thomas Nurthen; Timothy Gardam
Subject: Auto-microcons

Hi all
On the back of case manager's anecdotal feedback and our lab's second round of datamining of samples that underwent the auto-microcon process, an Options Paper was presented to QPS Superintendent of Forensic Services Dale Frieberg on ways forward for QPS to consider – continue with auto-microcon process, or cease auto-microcons.

QPS have advised the laboratory that they do not wish for our efforts to be put to the auto-microcon process (including the efforts in interpretation) for Priority 1 or 2 samples.

This means samples in the range 0.001ng/uL (LOD) - 0.0088ng/uL will be reported at Quant stage as 'DNA Insufficient for Further Processing'. This is consistent with the process in place for P3 samples. The manual Microcon process may be performed upon QPS request.

To report in a statement, the following wording could be used:

Low levels of DNA were detected in this sample and it was not submitted for further DNA profiling.

This is slightly different to the wording written in 2012/13 for these samples (P3) but after some consultation, appears a good starting point.

An enhancement has been requested to enable this to occur from 12 February. Reactivating samples for further post-extraction processing, if requested from QPS, will be directed to Luke via an FR Request. If there are changes to the 12 February date, I will let you know. As usual, appropriate comments to SOPs will follow.

Regards
Justin

Justin Howes
Team Leader – Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Forensic & Scientific Services,
Health Support Queensland, **Department of Health**
[redacted]

KDR-2

HealthSupport Queensland
Forensic and Scientific Services

Forensic DNA Analysis

Implementation Plan for 3500xL PowerPlex 21 Casework

Kylie Rika, 3 Dec 2020

Project Title: Implementation Plan for 3500xL PowerPlex®21 Casework Project Number: 230

Purpose

The purpose of this document is to highlight the items needing to be addressed prior to the implementation of the 3500xL Capillary Electrophoresis instrument for casework (CW) samples processed using the PowerPlex®21 (PP21) amplification kit.

Background

The Forensic DNA Analysis laboratory has recently prioritised the implementation of the 3500xL genetic analyser for PowerPlex®21 (PP21) Casework in response to the aging of the current Capillary Electrophoresis equipment (3130*xl*) and in line with the laboratory's Business Continuity Plan (BCP).

Scope

The scope of this document includes:

- A re-cap of work previously done looking into the use of the 3500xL as documented in Project # 186 (Assessment of 3500xL Analysis of Casework PowerPlex®21 samples using 3500xL A) and in the risk assessment for 3130*xl* including the recommendations and decisions made at the time
- A summary of recent work conducted under Project # 219 (Verification STRmix 2.7 for 3500xL), in particular with regards to the mixture assessment of PP21 CW baseline using DC4
- A summary of interpretation considerations
- A table including checklist items as part of the implementation plan for 3500xL PP21 CW
- A table including checklist item/s to form part of a post implementation review

Re-cap of work previously done

Project # 186 is an accumulation of a number of different projects and was initiated in an attempt to set conditions for the use of 3500xL for the analysis of casework samples amplified with PP21. Details of the work conducted under this project can be accessed within the report located in the change management folder (I drive). In summary, it was concluded that the implementation of the 3500xL A Genetic Analyzer coupled with PP21 was not preferred for routine case work and the following recommendations were put forward:

Recommendation 1

It is recommended that the 3500xL A Genetic Analyzer should not be implemented for routine casework sample processing at this time due to the interpretation difficulties associated to high peak heights and resultant elevated baseline, artefacts and pull-up particularly in the low molecular weight regions.

Recommendation 2

It is recommended that, if for business continuity reasons, the 3500xL A Genetic Analyzer is required to be implemented in combination with the PP21 amplification system for routine case work, that mixture samples be re-assessed using the loci specific stutter thresholds developed in project # 170 in conjunction with the use of the current STRmix version.

Recommendation 3

It is recommended that the use of stutter and sub threshold information in determining number of contributors needs to be assessed as part of supporting documentation for the implementation plan.

Recommendation 4

It is recommended that an interpretation and rework strategy be documented to assist with consistent interpretation.

These recommendations have either been mitigated due to the work done under Projects 219 and 230 or considered in this implementation plan (see checklist table below).

Summary of recent work conducted under Project # 219

Project # 219 has been broken down into three parts. Part A demonstrated that STRmix v2.7.0 has been verified for the interpretation of DNA profiles consisting of 1-3 contributors generated using PP21 and the 3500xL genetic analyser.

Part B demonstrated that the combined deconvolution of results obtained from the 3130*xl* and 3500xL are either equivalent to or better than the deconvolution of the individual profiles and therefore the combined kits function of STRmix v2.7.0 is considered suitable for use with combined 3130*xl* and 3500xL results.

Part C has verified the use of STRmix v2.7.0 for the interpretation of DNA profiles consisting of 4 contributors using PP21 and the 3500xL genetic analyser.

Baseline for 3500xL has been assessed as follows:

Baseline for *3500xL A PP21 Reference* was reviewed following a laser change in September 2019. The outcome of this review was that the previously implemented LOD and LOR thresholds were to be maintained (see I:\AAA Analytical\Audits and Reviews\AAA 3130-3500\Baseline Reviews\Review 3500A baseline post laser change 20191105\Final Report).

Baseline for 3500xL was further assessed for PP21 Casework DC4 as detailed at I:\Change Management\Proposal#230 - Implementation of 3500xL PP21 Casework\previous projects\Assessment of PowerPlex®21 Casework Baseline on 3500xL using Data Collection version 4.

The results of these assessments led to the following recommendations:
- Whole profile LOD/LOR to be used for ease of interpretation
- Implement DC4 for the analysis of PP21 samples on the 3500xL

These recommendations were endorsed by the management team and form part of this implementation plan.

Summary of interpretation considerations

Intuitive exclusions
- Drop-in parameters have been introduced into STRmix for the interpretation of 3500xL profiles meaning that a mismatch between a reference sample and a peak below the drop-in cap will not result in an exclusion; the probability of this peak being a drop-in peak will be factored into the calculated LR.
- The flow on effects of this are that a scientist will not be able to perform intuitive exclusions using peaks below the drop-in cap.
- It is agreed that intuitive exclusions cannot be performed on 3500xL profiles as detailed in I:\Change Management\Proposal#230 - Implementation of 3500xL PP21 Casework\ Decision Points Implementation Plan Discussion_20210106

Reproducibility
- The reproducibility guidelines were created to mitigate the risk of false exclusion where a ‘minor’ profile appeared to have one contributor where in fact it had two contributors. This risk may now be mitigated by the drop-in modelling.

Combined 3130xL and 3500xL profiles
- The scenario of an exclusionary sub-threshold peak on a 3130xL profile where a 3500xL profile is also available has been considered.
- It is agreed that if there are 3130xL and 3500xL profile/s for the same sample then 3500xL interpretation rules apply (I:\Change Management\Proposal#230 - Implementation of 3500xL PP21 Casework\ Decision Points Implementation Plan Discussion_20210106)

Use of sub-threshold peaks
- It is agreed that sub-threshold peaks are only to be used for assessment of the number of contributors (I:\Change Management\Proposal#230 - Implementation of 3500xL PP21 Casework\ Decision Points Implementation Plan Discussion_20210106)

It is the recommendation of the author to implement the 3500xL for PP21 Casework, with the following requirements:

Task	Details	Responsibility (line manager)	Date Completed
Forensic Register	Check/test that the import of data from Genemapper IDX to the Forensic Register works and that STRmix output files are suitable. Job #1788 has been added to Azure. Workaround is available if not complete before implementation.	Justin	Importing of data works. Work-around implemented. JAH 04/03/2021
	Log a job in Azure to ensure the casework samples are directed to the 3500xL for Capillary Electrophoresis. Change default on go-live date. Workaround is available.	Luke	User Story #1809 refers. Work around implemented. JAH 05/03/2021
	Job #1786 has been added to Azure to ensure QFLAG matching can occur as per requirements	Kirsten	In progress. Current QFLAG process can continue in the meantime. JAH 05/03/2021
	Log a job in Azure to request for the plate reading upload warning for stutter be removed	Megan	User Story #1788 refers. Work around implemented. JAH 05/03/2021
Plate Reading	Change to plate reading practice so that plate readers leave +1rpt stutter peaks labelled	Luke	Complete: Email from Megan Mathieson to plate readers 17/02/2021. JAH 05/03/2021
GeneMapper IDX	GMIDX print settings to be added for 400rfu zoom	Luke	Complete: Email from Megan Mathieson to plate readers 17/02/2021. JAH 05/03/2021
Interpretation	Reproducibility guidelines to be reviewed to ensure they fit with the interpretation of 3500xL profiles	Sharon	FRIT seniors meeting 29/01/2021. No need for reproducibility guidelines at this stage. JAH 04/03/2021

Information Materials	Create information materials (eg. presentations) for understanding Drop-in, combined stutter, combined kits functionality and interpretation, and changes to intuitive exclusions/use of sub-threshold peaks	Justin	Complete and available on MS Teams. JAH 04/03/2021
Update Standard Operating Procedures	QIS 35007 (STRmix)	Emma	Complete – comment added. JAH 05/03/2021
	QIS 17117 (Case management)	Justin	Complete JAH 04/03/2021
	QIS 33773 (PDA)	Angelina	Complete – comment added. JAH 05/03/2021
	QIS 34112 (GeneMapper)	Kerry-Anne	Complete JAH 05/03/2021
	Analytical SOPs: QIS 31514, QIS 34062, QIS 34052, QIS 17210, QIS 34045, QIS 33406, QIS 34131, QIS 34034, QIS 34112, QIS 34064	Belinda	QIS 31514 is not relevant. All other SOPs updated or have comments. JAH 05/03/2021
Information Sessions	Presentation to staff on Drop-in and how it impacts interpretation	Justin	Complete and available on MS Teams. JAH 04/03/2021
	Presentation to staff on changes to intuitive exclusions and use of sub-threshold peaks	Justin	Complete and available on MS Teams. JAH 04/03/2021
	Presentation to staff on how to change kit settings for each CE type (including Health Practitioner Officer 2 (HP2s))	Allan	Complete and available on MS Teams. JAH 04/03/2021
	Presentation to staff on the combined kits functionality and interpretation	Justin	Complete and available on MS Teams. JAH 04/03/2021
	Presentation to staff on how STRmix handles combined stutter	Justin	Complete and available on MS Teams. JAH 04/03/2021
	Presentation to Operational Officer (OO) staff concerning changes to zoom of	Kirsten	Complete – communication occurred

	electropherograms (epg's) (from 200rfu to 400rfu)		without the need for presentation. JAH 05/03/2021
	Workflow design needed to enable instructions from case managers to HP2's on dealing with combined kits – instructions go into PDA comments	Justin	Complete and available on MS Teams. JAH 04/03/2021
IT	3500xL STRmix settings to be added to all PCs	Justin or Erin	Complete JAH 04/03/2021
	Check the settings have been correctly applied	Justin	Challenge Testing - complete 10/003/2021
Communication	Reporters to be advised of modelling of post stutter and review of reproducibility guidelines	Justin	Complete and available on MS Teams. JAH 04/03/2021
	Dissemination of information relating to the move to PP21 on the 3500xL to all sub teams	Justin/Paula	Complete – email sent 09/02/2021 to confirm implementation will be 15/02/2021. JAH 05/03/2021
	Minor change register to be updated upon go-live date (01/02/2021)	Justin/Paula	Go-live was 15/02/2021. Minor change log updated. JAH 05/03/2021

It is a further recommendation of the author to consider conducting a post implementation review which could include (but not limited to):

Review quant range for DIFP process	Evaluate if the quant range still holds for defining DNA Insufficient for Further Processing (DIFP)	Justin/Allan	To be considered possibly at post-implementation review. JAH 05/03/2021

Acknowledgements:

Angela Adamson, Belinda Andersen, Emma Caunt, Cassandra James, Kerry-Anne Lancaster, Megan Mathieson, Chelsea Savage

Queensland Health
Forensic and Scientific Services

KDR-3

Forensic DNA Analysis Management Team Operational Focus Meeting – Minutes

Date: 11 November 2021
Time: 11:30am
Venue: Conf Room 103
Meeting Commenced at:

Name	Initials	Position	Attending
Committee Members			
Cathie ALLEN (Chair)	CJA	Managing Scientist, PSS	No
Justin HOWES (Chair)	JAH	A/Managing Scientist, PSS	Yes
Paula BRISOTTO	PMB	Team Leader, Forensic DNA Analysis	Yes
Sharon JOHNSTONE	SMJ	A/Team Leader, Forensic DNA Analysis	Yes
Allison LLOYD	AKL	Senior Forensic Scientist	Yes
Adrian Pippia	AAP	A/Senior Forensic Scientist	Yes
Kylie RIKA	KDR	Senior Forensic Scientist	Yes
Luke RYAN	LBR	Senior Forensic Scientist	Yes
Kirsten SCOTT	KDS	Senior Forensic Scientist	Yes
Wendy HARMER	WAH	Administration Support Officer	No
Participants			
Guests -			

Item	Topic	Lead	Paper Attached
1	**Welcome and apologies**	Chair	
1.1	**Acknowledgement of Country** I would like to acknowledge the Yuggera peoples and Turrbal peoples as the Traditional and Cultural Custodians of the lands upon which we meet today Meanjin Brisbane and pay respect to Elders past, present and emerging.	Chair	

1.2	**Confirmation of attendees and apologies**	Chair	N/A
2	**Review and acceptance of previous minutes and update on actions register**	Chair	
2.1	Minutes of previous meeting - Accepted via email 1 Nov 2021		
2.2	**Action Register:** **Forensic DNA Analysis Management Action Register**	Chair	See link for list
3	**Standing Agenda Items**		
3.1	**HR Update** HR Stats for October – will be available soon, WAH will send via email (WAH)	Mgmt Team	
3.2	**Workplace Health and Safety** 11/11/2021: Kristina on training to be the lab rep.	Mgmt Team	
3.3	**Operational Initiatives / Ideas** **Business cases**: **HTER**: one item outstanding - StorStar **Capital funding:** Request for funding for a walk-in Freezer	Mgmt Team	
3.4	**Teams Updates around Workflow Impacts, Risks & Mitigation** Team wins: Tip box basketball; EOI for CA closes 11/11/2021 Current Priorities: Nothing noted. Team challenges and impacts: FR downtime, URL unavailability. KDR: TAT impacts – P1 cases, defence requests, court appearances, higher duties, validation and project work. JAH: Most of these impacts have been communicated to A/ED Lara Keller and QPS and acknowledged. Performance: (KPIs etc) Nothing noted.	Mgmt Team	
3.5	**Communications from relevant meetings** - Quality Community of Practice (QCoP) – nil to update - FSS Leadership meeting –	Mgmt Team	

	Finance: all HTER items should be purchased by Dec 2021, if this is unable to be achieved, please advise Gemma Mockler on the possible date of purchase. HR: Mandatory COVID vaccinations for QH staff in clinical care environments, FSS staff are encouraged to add their COVID vaccination certificate to the Hub. QIRC made a ruling on the 20/21 State wage increase and this will be applied from Sept 2021 (2.5%). WfQ Survey results are in and Lara Keller discussed FSS results on Monday 1st of Nov. Team results supplied to management team after that meeting. Safety – still some areas of FSS that are required to complete the FSS Hazard Register – has Forensic DNA Analysis completed this? SMJ- perhaps something the new OHS delegate could look into? Minor update on Business Case for Significant Change – it is a whole of PQFSS approach, there are some proposed structural changes and some proposed reviews to look at longer term items. A/EDFSS will discuss these with the relevant affected direct reports prior to wider communication. No further detail has been provided on this. - FSS/FSG meeting – Nil - FSS/FSG re: FR – Nil - Other – Human Ethics Committee (KDS) – first meeting attended but nil to update relevant to Forensic DNA Analysis.		
3.6	**Budget –** Chair At the end of September, Forensic DNA Analysis overspent by $51,000		

Profit and Loss Report (All)

	Sept 21 Actual	Sept21 Budget	Variance	YTD Actual	YTD Budget	YTD Variance	Full Year Budget
Revenue	**-348,020**	**-378,508**	**-30,488**	**-1,114,565**	**-1,135,524**	**-20,959**	**-4,543,731**
User Charges	-348,020	-378,508	-30,488	-1,114,565	-1,135,524	-20,959	-4,543,731
Labour Expenses	**624,978**	**626,289**	**1,312**	**1,858,379**	**1,835,505**	**-22,874**	**7,408,463**
Labour - Health Practitioners	541,163	538,283	-2,881	1,601,234	1,577,612	-23,621	6,377,559
Labour - Managerial & Clerical	28,826	27,010	-1,816	82,307	78,312	-3,995	311,944
Labour - Operations					0	0	0
Labour Related Taxes	146		-146	438		-438	
Other Employee Related Expenses				427		-427	
Workcover Premiums	1,912	1,756	-156	5,467	5,268	-199	21,072
Labour-Clinical Assistants	52,930	59,240	6,311	168,507	174,313	5,806	697,888
Non Labour Expenses	**148,615**	**161,975**	**13,360**	**498,621**	**490,925**	**-7,696**	**2,014,707**
Building Services	1,081	0	-1,081	1,081	4,200	3,119	16,400
Catering And Domestic	1,218	1,333	115	5,222	3,999	-1,223	15,996
Clinical Supplies	119,101	129,671	10,570	396,359	389,013	-7,346	1,556,049
Communication	1,756	1,827	71	5,483	5,481	-2	21,924
Computers	10,099	7,391	-2,708	32,150	21,973	-10,177	137,992
Non Capitalised Asset Related Costs		0	0	3,761	1,000	-2,761	5,000
Other Supplies And Services	810	690	-120	3,594	2,070	-1,524	8,590
Travel Expenses	69		-69	100		-100	
Repairs And Maintenance	14,440	21,063	6,623	50,196	63,189	12,993	252,756
Repairs And Maintenance - Building				637		-637	
Miscellaneous	40		-40	40		-40	
Depreciation	**23,287**	**23,367**	**80**	**71,414**	**71,660**	**246**	**284,303**
Depreciation & Amortisation	23,287	23,367	80	71,414	71,660	246	284,303
Operating Position (Surplus)/Deficit	**448,860**	**433,124**	**-15,736**	**1,313,850**	**1,262,566**	**-51,284**	**5,163,742**

4	**Project Updates**		
	Project updates provided prior to meeting and the updated below to be read prior to the meeting. Any significant progress to be discussed. Weeks of nil update to be tracked.		
4.1	**Project #199 Validation of Proflex** 10/11/2021 - Report with Mgt Team for review 11/11/2021: LBR: feedback focus mainly on stutter data – the limited number of samples/data size can affect SD. What do we want to see in the experimentt? Perhaps looking at how much of the data is over current threshold? Ie. Tally the numbers and loci where over the existing thresholds. Noted that there was data below threshold as well. Aim of testing was to see if the values were similar between each other, and comparable to 9700. Any proposed alternatives to look at this data, please speak to LBR.	LBR	
4.2	**Project # 206 – Y Filer Plus** *To be reviewed at both Strategy & Operational Meetings* 09/11/2021 - TEN, KDS and KDR having MS Teams meeting with AFP next week (90min session to receive YSTR FR demo and chat). Sharelle making up mixtures in the lab. Some YPWG email discussions centred on the following	KDR	

	questions: How do you report Y database links (both when autosomal info supports or doesn't support the link)? Do you report Y links with one mismatch (e.g. as a possible familial link)? Does this link get reported even if an autosomal familial search has not been done? If there is one Y mismatch and the familial search has been done but has not linked the samples does the Y mismatch get reported?		
4.3	**Project #213 – Verifiler Plus** 09/11/2021 – 1. *Testing the Impact of Pre-Prepared VeriFiler™ Plus PCR Amplification Reagents on PCR Efficiency and Quality.* Primary author - CKS. - Finalised 2. *Testing of VeriFiler™ Plus PCR Amplification Reagent Stability at Room Temperature* Primary author - CKS. Final report with Verifiler team for review. - Finalised 3. *VeriFiler™ Plus – Full Volume Amplification*. Primary author - LMF. - Finalised 4. *VeriFiler™ Plus – Stutter*. Primary author - CLJ. **Management has reviewed,** back for additional edits post feedback 5. *VeriFiler™ Plus – Direct Amplification*. Primary author - AF. Drafted report: with Luke and Megan for review before going to VF team for review 6. *VeriFiler™ Plus – Half Volume Amplification*. Primary author - Revised estimated date to provide report to VF team ~ before Christmas 7. *VeriFiler™ Plus – Testing for D10S1248*. Primary author - MMA. Submitted to VF feedback completed by 21st Oct. Pending edits and to management team this week 8. *VeriFiler™ Plus – STRmix*. Primary author - EJC. Still pending analysis of data. 9. *VeriFiler™ Plus – Mixtures*. Primary author - SMJ. Still pending analysis of data	KDS	
4.4	**Project #216 – Validation of Ion Chef and S5** *To be reviewed at both Strategy & Operational Meetings* 10/11/2021 - Training this week. EOI for PQ progressing. EOI at QEII out.	LBR	
4.5	**Project #221 – Impact of magnetic fingerprint powders on bead-based trace DNA extraction (collab with QPS)** 10/11/2021 - Exp Design in draft.	LBR	
4.6	**Project #227 – Baseline Method Trial** 11/11/2021: nil update	PMB	

4.7	**Project #229 – Paternity Index Distributions in PP21** 09/11/2021 – report is written and with JAH for review before going to the mgt team.	SMJ	
4.8	**Project #233 – Bone sampling and demineralisation protocol** 10/11/2021 – nil update	AKL	
4.9	**Project #234 – Process mapping of interpretation and reporting (SMJ)** 09/11/2021 – It's on hold at the moment	SMJ	
4.10	**Project #235 - 2021 FR version upgrade**	Mgmt Team	
4.11	**Project #236 – Exhibit Result Line Revision** 11/11/2021: To close this project as it now will roll into FR version upgrade.	JAH	
5	**Projects on Hold – to be reviewed at Strategy focussed meeting as well**		
	Nil		
6	**Matters for discussion / decision**		
6.1	Requests/suggestions for audit topics 2022 (KDS) 11/11/2021: some previous suggestions to follow, possibly in 2023 include – VFP, Proflex, NIFA. Suggestions: audit Difference of Opinion Process, lubricant testing process, continuity of samples, equipment and calibrations, statement production via paperless process. Any more to KDS please.		
7	**Matters for noting**		
7.1	**ANZFSS 25th International Symposium call for Abstracts:** https://www.anzfss2022.com/submit-abstract/ Invitation for submission of abstracts for original work (either Oral presentation or Poster presentation): **Submission date is Monday 7 February 2022.**	JAH	

	Author notifications: April 2022.		
7.2	**Familial Testing challenge in South Australia** Challenge heard in a Voir Dire that took evidence from Dr Duncan Taylor. Challenge included legality of familial search using covert sample. Pending voir dire decision, familial testing has been halted at FSSA. The testing was not via NIFA, was performed during a trial of using familial searches more proactively. DNA results (not familial results yet) are able to proceed to committal.	JAH	
8	**Other Business**		
8.1	**DNA Insufficient for Processing (DIFP) process** KDR collecting samples where better results obtained after case manager requested concentration, including profiles for NCIDD. General discussion ensued that this possibility was communicated and accepted by QPS, and that they could request processing any time and that the case manager may rework if case circumstances indicate worthwhile. Value for DIFP determined from PCR (PP21 validation); values may be different with VFP which is more sensitive. Suggestion from LBR that may be worthwhile if moving to VFP that we profile above this value and then after collecting enough data (eg. last data was a year of data), review the findings to see if a threshold could be determined. KDS mentioned if collecting data, need to balance with the number that do not eventuate with profiles (as many get requested by QPS monthly for reactivation).	KDR	

Next Meeting: Thursday 25 November 2021

KDR-4

Kylie Rika

From: Justin Howes
Sent: Thursday, 10 February 2022 12:23 PM
To: Kylie Rika
Subject: RE: DIFP

Hi Kylie, no there is no movement on reassessing quant ranges to my knowledge. I am aware that there were a large number of further processing requests from QPS and FSS in this matter, which is showing a good use of the FR and rework decisions. There are a variety of outcomes as expected as well.

What do you think Claire means by 'backlash'? Is this just a turn of phrase or something?

Justin

Justin Howes
Team Leader - Forensic Reporting and Intelligence Team

Forensic DNA Analysis, Police Services Stream, Forensic & Scientific Services
Prevention Division, Queensland Health

[redacted]

Please note that I may be working from a different location during the COVID-19 Pandemic. The best contact method is via email.

Queensland Health acknowledges the Traditional Owners of the land, and pays respect to Elders past, present and emerging.

From: Kylie Rika <Kylie.Rika@health.qld.gov.au>
Sent: Thursday, 10 February 2022 12:09 PM
To: Justin Howes <[redacted]>
Subject: FW: DIFP

Hi Justin

I haven't replied to Claire yet. Before I do, I just wanted to check that there hasn't been any more movement on re-assessing quant ranges for DIFP process. I think we last talked about this in the mgmt. team meeting on 11 November 2021 Ops meeting?

What wasn't included in the minutes was the discussion around the fact that we need QPS/BDNA to do the data dump for us which could be challenging due to cost involved etc….

Thanks

Kylie

From: Claire Gallagher <[redacted]>
Sent: Thursday, 10 February 2022 9:06 AM
To: Kylie Rika <[redacted]>
Subject: RE: DIFP

No. Its not a new upload or anything, so no immediate backlash. It's the same SS profile that's on that same item. Just highlighting that maybe we need to look into our quants for DIFP. Sorry I didn't include the barcode.

[redacted]

Thanks,
Claire

From: Kylie Rika <[redacted]>
Sent: Thursday, 10 February 2022 8:55 AM
To: Claire Gallagher <[redacted]>
Subject: RE: DIFP

Thanks Claire

Was this a new "result" for the case?

From: Claire Gallagher <[redacted]>
Sent: Wednesday, 9 February 2022 3:09 PM
To: Kylie Rika <[redacted]>
Subject: DIFP

Hi Kylie

This sample from Adrian's P1 case was DIFP. It got reworked and has come back as a 20L profile matching a ref sample. The quant was on the high side, but given it was DIFP, it wouldn't have been considered for a rework initially. It was 0.00783ng/uL.

Thanks,
Claire

Claire Gallagher
Scientist - Forensic Reporting and Intelligence Team

Forensic & Scientific Services
Prevention Division, Queensland Health

[redacted]

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CLEAN HANDS
SAVE LIVES
Wash your hands regularly
to stop the spread of germs.

KDR-5

Kylie Rika

From: Kylie Rika
Sent: Thursday, 28 April 2022 2:51 PM
To: Paula Brisotto
Subject: RE: Testing restarted process improvement
Attachments: DIFP Nov 2021 as at 28 April 2022.xlsx

Hi Paula

I am just wondering if the data grab from FR has been received yet? Depending on the search parameters that were requested, I am wondering if we could possibly also use the data in a post implementation review of the DIFP process. From the mgmt. meeting on the 11 Nov 2021, I raised the following:

DNA Insufficient for Processing (DIFP) process

KDR collecting samples where better results obtained after case manager requested concentration, including profiles for NCIDD. General discussion ensued that this possibility was communicated and accepted by QPS, and that they could request processing any time and that the case manager may rework if case circumstances indicate worthwhile. Value for DIFP determined from PCR (PP21 validation); values may be different with VFP which is more sensitive.

Suggestion from LBR that may be worthwhile if moving to VFP that we profile above this value and then after collecting enough data (eg. last data was a year of data), review the findings to see if a threshold could be determined.

KDS mentioned if collecting data, need to balance with the number that do not eventuate with profiles (as many get requested by QPS monthly for reactivation).

I have attached the collection of samples so far.

This s/sheet was set up so that instead of staff emailing me or Adrian (at the time) with samples they wanted to bring to our attention (as examples of DIFP that then ended up in a good result), they could just add to this s/sheet.

I realise this s/sheet is not a balanced collection so we cannot derive any trends etc., but some of the info in it has made me think, we really need to review this process and the quant ranges used to drive DIFP.

I am aware of a lot more examples that people have in their large cases that they haven't yet had a chance to add to the s/sheet.

Happy to discuss further in person if you like.

Thanks

Kylie

From: Paula Brisotto <[redacted]>
Sent: Thursday, 3 March 2022 2:08 PM

To: Kylie Rika <[redacted]>
Subject: RE: Testing restarted process improvement

Thanks for the extra information Kylie.

A data grab has been requested from the FR which may have information in it that could be used to inform next steps for this. Once this data is received, we will know more about what we can assess from it.

I think after this is done and depending on what can be determined, it would be a good time for you, Sharon and Justin to discuss the benefits of a list that FRIT will manage and assess for these reworks.

Thanks,
Paula

From: Kylie Rika <[redacted]>
Sent: Thursday, 3 March 2022 1:10 PM
To: Paula Brisotto <[redacted]>
Subject: RE: Testing restarted process improvement

Hi Paula,

I am thinking that they go onto a list for a CMer to consider any RW option. A CMer may want to consider a re-quant first for example. Or if the quant is just under 0.008 then try amp at max etc….

So I'm proposing they go to a list for a CMer to consider any testing option not just mic to 30 or mic to full.

Thanks
Kylie

From: Paula Brisotto <[redacted]>
Sent: Thursday, 3 March 2022 11:55 AM
To: Kylie Rika <[redacted]>
Subject: RE: Testing restarted process improvement

Hey Kylie,

Sorry for following up as I realise this is a crazy week. Are you able to provide more info on the below?

Thanks,
Paula

From: Paula Brisotto
Sent: Monday, 28 February 2022 10:31 AM
To: Kylie Rika <[redacted]>
Subject: RE: Testing restarted process improvement

Hi Kylie,

In order to help determine next steps, can I clarify if the assessment by case managers is to determine if a full microcon or microcon to 30 is required?

Thanks
Paula

From: Kylie Rika <[redacted]>
Sent: Tuesday, 22 February 2022 2:27 PM
To: Paula Brisotto <[redacted]>
Subject: No, I don't support this: Testing restarted process improvement

Hi Paula

I would like ALL (internal and QPS) initiated further processing requests to go onto a list that CMers can assess and address.

Thanks
Kylie

KDR-6

Kylie Rika

From: Kylie Rika
Sent: Friday, 24 June 2022 2:05 PM
To: Paula Brisotto
Subject: RE:

Hi Paula

As per the mgmt. meeting minutes from Nov 2021, I asked Ingrid to add it to the s/sheet at G:\ForBiol\AAA Forensic Reporting & Intel\DIFP 2021 examples. I haven't had anyone ask me to stop adding to this s/sheet so hope this is OK.

This sample is really, just an example of Q. 0.004 and good profile obtained loaded to NCIDD.

Agree that the current process worked, but I still worry about the situation where we amp those under 0.0088 at 15ul straight up without the chance to consider m'con first (15ul of our extract is gone – which means less extract to concentrate). In this sample ([redacted]), we have also added an extra step in the processing – increasing the chance of more sample waste and extra step to possibly expose to contamination.

As Cathie mentioned at our mgmt. meeting, this new process is a government decision that was made after she presented them the options if we remove the DIFP. So I know there is probably not much we can do about it – I just wanted to raise my concern regardless.

Thanks
Kylie

From: Paula Brisotto <[redacted]>
Sent: Friday, 24 June 2022 1:46 PM
To: Kylie Rika <[redacted]>
Subject: RE:

Hi Kylie,

Thanks! This seems to be a great example of the process working and the case manager evaluating an appropriate rework strategy based on the initial profile obtained.

Is this being recorded somewhere, or just for noting? (sorry, not sure if I'm supposed to do anything further with this)

Thanks,
Paula

From: Kylie Rika <[redacted]>
Sent: Friday, 24 June 2022 12:41 PM
To: Paula Brisotto <[redacted]>
Subject: FW:

Hi Paula

In Justin's absence, please note this example.

Thanks
Kylie

From: Ingrid Moeller <[redacted]>
Sent: Friday, 24 June 2022 12:30 PM
To: Kylie Rika <[redacted]>
Subject:

Hi Kyles,

Re[redacted]- one of the DIFP samples originally amped at 15uls – sort of crappy profile, then I microconed to full and there will be a new upload.

Ingrid Moeller
Scientist

Forensic & Scientific Services
Prevention Division, Queensland Health

[redacted]w www.health.qld.gov.au/fss

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